AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the applications:

Listing of Claims:

Please cancel claims 1-31.

32.(New) A method of distinguishing between at least 25 different serotypes of *Streptococcus pneumoniae* in a sample, the method comprising,

i) analysing at least a portion of the nucleotide sequence between the 3' end of the *cpsA* gene and the 5' end of the *cpsB* gene, and/or

ii) analysing at least a portion of the *wzy* and/or *wzx* gene(s).

33. (New) The method of claim 32 which distinguishes between at least 70 different serotypes of *Streptococcus pneumoniae* in a sample.

34. (New) A method of determining the serotype of *Streptococcus pneumoniae* in a sample, the method comprising,

i) analysing at least a portion of the nucleotide sequence between the 3' end of the *cpsA* gene and the 5' end of the *cpsB* gene, and/or

ii) analysing at least a portion of the *wzy* and/or *wzx* gene(s).

35. (New) The method of claim 34, wherein the serotype is selected from the group consisting of: 2, 7A, 7B, 7C, 9A, 9L, 10F, 10A, 10B, 10C, 11F, 11A, 11B, 11C, 11D, 12F, 12A, 12B, 13, 15F, 15A, 15B, 15C, 16A, 17F, 17A, 18F, 18A, 18B, 21, 22F, 22A, 24F, 24A, 24B, 25F, 25A, 27, 28F, 28A, 31, 32F, 32A, 33F, 33A, 33B, 33C, 33D, 34, 35A, 35B, 35C, 36, 37, 38, 39, 40, 41F, 41A, 42, 43, 44, 45, 46, 47, 47A and 48.

36. (New) The method of claim 34, wherein the portion of the nucleotide sequence between the 3' end of the *cpsA* gene and the 5' end of the *cpsB* gene which is analysed is any nucleotide which is polymorphic between at least some of the *S. pneumoniae* serotypes referred to in Figure 2.

37. (New) The method of claim 34, wherein the method comprises amplifying at least a portion of the nucleotide sequence between the 3' end of the *cpsA* gene and the 5' end of the *cpsB* gene, and sequencing the amplification product.

38. (New) The method of claim 37, wherein the entire approximately 800 bp region as provided in Figure 2 is amplified and sequenced.

39. (New) The method of claim 38, wherein the amplification is performed using primer pairs comprising a sequence selected from the group consisting of:

1) GGCATT(/C)TATGGAGTTGATTCG(/A)TCCATT(/C)CACAC(C/T)TTAG (SEQ ID NO:68) and
GC(/T)TCAATG(/A)TGG(/A)GCAATG(/T)ACTGGA(/C)GTA(/G)ATTCCCA(/G)ACATC (SEQ ID NO:73) ,

2) GGCATT(/C)TATGGAGTTGATTCG(/A)TCCATT(/C)CACACC(/T) TTAG (SEQ ID NO:68) and
CCATCAC(/T)ATAGAGGTTAC(/A)TG(/A)TCTGGCATT(/C)GC (SEQ ID NO:71),

3) GAAAGTGGG(/A/T)GGG(/A/T)A(/G)A(/C)T(/G)TAT(/C)AAAGTA(/G) AATTCT(/G)CAAGAT(/C)TTA(/G)AAA(/G)G (SEQ ID NO:70) and
T(/G)CATG(/A)CTA(/G)AAC(/T)TCT(/A)ATC(/T)AAG(/A)GCATAACGACTATC(/T) (SEQ ID NO:72), and

4) primer pairs that amplify the same region, or diagnostic portion thereof, from the genome of a strain of *S. pneumoniae* as the primers provided in 1) to 3).

40. (New) The method of claim 34, wherein the nucleotide sequence analysis step comprises determining whether a polynucleotide obtained from *S. pneumoniae* selectively hybridises to a polynucleotide probe comprising one or more polymorphic regions of the nucleotide sequence between the 3' end of the *cpsA* gene and the 5' end of the *cpsB* gene, wherein such polymorphic regions are shown in Figure 2.

41. (New) The method of claim 40, wherein the nucleotide sequence analysis step comprises a plurality of said polynucleotide probes.

42. (New) The method of claim 40, wherein the polynucleotide probe(s) is present as a microarray.

43. (New) The method of claim 34 which comprises amplifying at least a portion of the *wzy* and/or *wzx* gene(s), and determining the length of the amplification product.

44. (New) The method of claim 43, wherein at least a portion of the *wzy* and/or *wzx* gene(s) is amplified using a primer comprising a sequence selected from any one of SEQ ID NO's 75 to 139 or 144 to 333, or a primer that can be used to amplify the same region, or diagnostic portion thereof, from the genome of a strain of *S. pneumoniae* as a primers provided as any one of SEQ ID NO's 75 to 139 or 144 to 333.

45. (New) A method of identifying serotype 3 of *Streptococcus pneumoniae* in a sample comprising performing a method of claim 34, and analysing the *orf2 (wze)-cap3A-cap3B* region.

46. (New) The method of claim 45, wherein the *orf2 (wze)-cap3A-cap3B* region is analysed by amplifying a portion of the *orf2 (wze)-cap3A-cap3B* region using primer pairs selected from the group consisting of:

1) GCACAAAAAAAAGTTTGATATTCCCCTTGACAATAG (SEQ ID NO:140) and GCAGGATCTAAGGAGGCTTCAAGATTCAACTC (SEQ ID NO:141),

2) CGAACCTACTATTGAGTGTGATACTTTTATGGGATACAGAG (SEQ ID NO:142) and CTGACAGCATGAAAATATATAACCGCCCAACGAATAAG (SEQ ID NO:143), and

3) primer pairs that amplify the same region, or diagnostic portion thereof, from the genome of a strain of *S. pneumoniae* as the primers provided in 1) or 2).

47. (New) The method of claim 32, the method further comprising detecting any serotype of *Streptococcus pneumoniae* in the sample.

48. (New) The method of claim 47, wherein the *psaA* and/or pneumolysin genes, or a portion thereof, is amplified.

49. (New) The method of claim 48, wherein a portion of the *psaA* gene is amplified using primers comprising the sequence TACATTACTCGTTCTCTTTCTTTCTGCAATCATTCTTG (SEQ ID NO:64) and TAGTAGCTGTCGCCTTCTTTACCTTGTTCTGC (SEQ ID NO:65), or primer pairs that amplify the same region, or diagnostic portion thereof, from the genome of a strain of *S. pneumoniae* as SEQ ID NO:64 and SEQ ID NO:65.

50. (New) The method of claim 48, wherein a portion of the pneumolysin gene is amplified using primers comprising the sequence AGAATAATCCCACTCTTCTTGCGGTTGA (SEQ ID NO:66) and CATGCTGTGAGCCGTTATTTTTTCATACTG (SEQ ID NO:67) or primer pairs that amplify the same region, or diagnostic portion thereof, from the genome of a strain of *S. pneumoniae* as SEQ ID NO:66 and SEQ ID NO:67.